

INSB

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: JOHNSON, EUGENE M
MILBRANDT, JEFFREY D
KOTZBAUER, PAUL T
LAMPE, PATRICIA A
KLEIN, ROBERT
DESAUVAGE, FRED
- (ii) TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
- (iii) NUMBER OF SEQUENCES: 239
- (iv) CORRESPONDENCE ADDRESS:
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(E) COUNTRY: USA
(F) ZIP: 63105
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: HOLLAND, DONALD R.
(B) REGISTRATION NUMBER: 35,197
(C) REFERENCE/DOCKET NUMBER: 971486
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala	Arg	Leu	Gly	Ala	Arg	Pro	Cys	Gly	Leu	Arg	Glu	Leu	Glu	Val	Arg
1				5					10					15	
Val	Ser	Glu	Leu	Gly	Leu	Gly	Tyr	Ala	Ser	Asp	Glu	Thr	Val	Leu	Phe
			20					25						30	

Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp Leu
 35 40 45
 Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg Val
 50 55 60
 Arg Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser
 65 70 75 80
 Phe Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser Ala
 85 90 95
 Arg Glu Cys Ala Cys Val
 100

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Pro Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser
 1 5 10 15
 Glu Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr
 20 25 30
 Cys Ala Gly Ala Cys Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu
 35 40 45
 Arg Arg Leu Arg Gln Arg Arg Arg Val Arg Arg Glu Arg Ala Arg Ala
 50 55 60
 His Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu
 65 70 75 80
 Asp Val His Ser Arg Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu
 85 90 95
 Cys Ala Cys Val
 100

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser Gly Ala Arg Pro Xaa Gly Leu Arg Glu Leu Glu Val Ser Val Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "SERINE OR CYSTEINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Xaa Cys Ala Gly Ala Xaa Glu Ala Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /note= "GLUTAMINE OR GLUTAMIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Xaa Xaa Val Glu Ala Lys Pro Cys Cys Gly Pro Thr Ala Tyr Glu Asp
1 5 10 15

Xaa Val Ser Phe Leu Ser Val
20

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Tyr His Thr Leu Gln Glu Leu Ser Ala Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 197 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser
1 5 10 15
Val Leu Ser Ile Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg
20 25 30
Leu Gly Pro Ala Leu Val Pro Leu His Arg Leu Pro Arg Thr Leu Asp
35 40 45
Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
50 55 60
Pro Asp Ala Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro
65 70 75 80
Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg Ala
85 90 95
Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val
100 105 110
Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu Phe Arg
115 120 125
Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp Leu Gly
130 135 140
Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg Val Arg
145 150 155 160

[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCGCGGTTGG GGGCGCGGCC TTGCGGGCTG CGCGAGCTGG AGGTGCGCGT GAGCGAGCTG	60
GGCCTGGGCT ACGCGTCCGA CGAGACGGTG CTGTTCCGCT ACTGCGCAGG CGCCTGCGAG	120
GCTGCCGCGC GCGTCTACGA CCTCGGGCTG CGACGACTGC GCCAGCGGCG GCGCCTGCGG	180
CGGGAGCGGG TGC GCGCGCA GCCCTGCTGC CGCCCGACGG CCTACGAGGA CGAGGTGTCC	240
TTCTTGACG CGCACAGCG CTACCACAG GTGCACGAGC TGTCGGCGCG CGAGTGCGCC	300
TGCGTG	306

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCGGGGGCTC GGCCTTGTGG GCTGCGGAG CTCGAGGTGC GCGTGAGCGA GCTGGGCCTG	60
GGCTACACGT CGGATGAGAC CGTGCTGTC CGCTACTGCG CAGGCGCGTG CGAGGCGGCC	120
ATCCGCATCT ACGACCTGGG CCTTCGGGCG CTGCGCCAGC GGAGGCGCGT GCGCAGAGAG	180
CGGGCGCGGG CGCACCCGTG TTGTCGCCCG ACGGCCTATG AGGACGAGGT GTCCTTCCTG	240
GACGTGCACA GCCGCTACCA CACGCTGCAA GAGCTGTCGG CGCGGGAGTG CGCGTGCGTG	300

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 591 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGCAGCGCT GGAAGGCGGC GGCCTTGGCC TCAGTGCTCT GCAGTCCGT GCTGTCCATC	60
TGGATGTGTC GAGAGGGCCT GCTTCTCAGC CACCGCCTCG GACCTGCGCT GGTCCCCCTG	120
CACCGCCTGC CTCGAACCCT GGACGCCCCG ATTGCCCGCC TGGCCAGTA CCGTGCACTC	180

CTGCAGGGGG CCCCGGATGC GATGGAGCTG CGCGAGCTGA CGCCCTGGGC TGGGCGGCCC 240
 CCAGGTCCGC GCGTCGGGC GGGGCCCCGG CGGCGGCGCG CGCGTGCGCG GTTGGGGGCG 300
 CGGCCTTGCG GGCTGCGCGA GCTGGAGGTG CGCGTGAGCG AGCTGGGCCT GGGCTACGCG 360
 TCCGACGAGA CGGTGCTGTT CCGCTACTGC GCAGGCGCCT GCGAGGCTGC CGCGCGCGTC 420
 TACGACCTCG GGCTGCGACG ACTGCGCCAG CGGCGGCGCC TCGGCGGGGA GCGGGTGCGC 480
 GCGCAGCCCT GCTGCCGCC GACGGCCTAC GAGGACGAGG TGTCTTCCT GGACGCGCAC 540
 AGCCGCTACC ACACGGTGCA CGAGCTGTCG GCGCGCGAGT GCGCCTGCGT G 591

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 585 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGAGGCGCT GGAAGGCAGC GGCCCTGGTG TCGCTCATCT GCAGCTCCCT GCTATCTGTC 60
 TGGATGTGCC AGGAGGGTCT GCTCTTGGGC CACCGCCTGG GACCCGCGCT TGCCCCGCTA 120
 CGACGCCCTC CACGCACCTT GGACGCCCGC ATCGCCCGCC TGGCCCAGTA TCGCGCTCTG 180
 CTCCAGGGCG CCCCCGACGC GGTGGAGCTT CGAGAAGTTT CTCCCTGGGC TGCCCGCATC 240
 CCGGGACCGC GCCGTCGAGC GGGTCCCCGG CGTCGGCGGG CGCGGCCGGG GGCTCGGCCT 300
 TGTGGGCTGC GCGAGCTCGA GGTGCGCGTG AGCGAGCTGG GCCTGGGCTA CACGTCCGAT 360
 GAGACCGTGC TGTTCCGCTA CTGCGCAGGC CCGTGCGAGG CGGCCATCCG CATCTACGAC 420
 CTGGGCCTTC GGCCTGCGC CCAGCGGAGG CCGTGCGCA GAGAGCGGGC GCGGGCGCAC 480
 CCGTGTTGTC GCCCGACGGC CTATGAGGAC GAGGTGTCCT TCCTGGACGT GCACAGCCGC 540
 TACCACACGC TGCAAGAGCT GTCGGCGCGG GAGTGCCTG GCGTG 585

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGAGGGAGAG CGCGCGGTGG TTTCGTCCGT GTGCCCCGCG CCCGGCGCTC CTCGCGTGGC 60
 CCCGCGTCCT GAGCGCGCTC CAGCCTCCCA CGCGCGCCAC CCCGGGGTTC ACTGAGCCCG 120

GCGAGCCCGG GGAAGACAGA GAAAGAGAGG CCAGGGGGGG AACCCCATGG CCCGGCCCGT 180
 GTCCCGCACC CTGTGCGGTG GCCTCCTCCG GCACGGGGTC CCCGGGTCGC CTCCGGTCCC 240
 CGCGATCCGG ATGGCGCACG CAGTGGCTGG GGCCGGGCCG GGCTCGGGTG GTCGGAGGAG 300
 TCACCACTGA CCGGGTCATC TGGAGCCCGT GGCAGGCCGA GGCCCAGG 348

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTACCTCA CGCCCCCGA CCTGCGAAAG GGCCCTCCCT GCCGACCCTC GCTGAGAACT 60
 GACTTCACAT AAAGTGTGGG AACTCCC 87

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser
 1 5 10 15
 Val Leu Ser

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Arg Arg Trp Lys Ala Ala Ala Leu Val Ser Leu Ile Cys Ser Ser
 1 5 10 15
 Leu Leu Ser

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGCAGCGCT GGAAGGGGC GGCCTGGCC TCAGTGCTCT GCAGTCCGT GCTGTCC

57

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATGAGGCGCT GGAAGGCAGC GGCCTGGTG TCGTCATCT GCAGTCCCT GCTATCT

57

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ile	Trp	Met	Cys	Arg	Glu	Gly	Leu	Leu	Leu	Ser	His	Arg	Leu	Gly	Pro
1				5					10					15	
Ala	Leu	Val	Pro	Leu	His	Arg	Leu	Pro	Arg	Thr	Leu	Asp	Ala	Arg	Ile
			20					25					30		
Ala	Arg	Leu	Ala	Gln	Tyr	Arg	Ala	Leu	Leu	Gln	Gly	Ala	Pro	Asp	Ala
			35				40					45			
Met	Glu	Leu	Arg	Glu	Leu	Thr	Pro	Trp	Ala	Gly	Arg	Pro	Pro	Gly	Pro
	50					55					60				
Arg	Arg	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Arg	Ala	Arg				
	65					70					75				

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

ATCTGGATGT GTCGAGAGGG CCTGCTTCTC AGCCACCGCC TCGGACCTGC GCTGGTCCCC      60
CTGCACCGCC TGCCTCGAAC CCTGGACGCC CGGATTGCCC GCCTGGCCCA GTACCGTGCA      120
CTCCTGCAGG GGGCCCCCGA TGCGATGGAG CTGCGCGAGC TGACGCCCTG GGCTGGGCGG      180
CCCCAGGTC CGCGCCGTCG GCGGGGGCCC CGCGGCGGCG GCGCGCGT      228
  
```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

GTCTGGATGT GCCAGGAGGG TCTGCTCTTG GGCCACCGCC TGGGACCCGC GCTTGCCCCG      60
CTACGACGCC CTCCACGCAC CCTGGACGCC CGCATCGCCC GCCTGGCCCA GTATCGCGCT      120
CTGCTCCAGG GCGCCCCCGA CGCGGTGAG CTCGAGAAC TTTCTCCCTG GGCTGCCCCG      180
ATCCCGGGAC CGCGCCGTCG AGCGGGTCCC CGCGCTCGGC GGGCGCGG      228
  
```

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Val Trp Met Cys Gln Glu Gly Leu Leu Leu Gly His Arg Leu Gly Pro
 1           5           10           15
Ala Leu Ala Pro Leu Arg Arg Pro Pro Arg Thr Leu Asp Ala Arg Ile
          20           25           30
Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala Pro Asp Ala
          35           40           45
Val Glu Leu Arg Glu Leu Ser Pro Trp Ala Ala Arg Ile Pro Gly Pro
          50           55           60
  
```

Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser
1 5 10 15
Val Leu Ser Ile Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg
20 25 30
Leu Gly Pro Ala Leu Val Pro Leu His Arg Leu Pro Arg Thr Leu Asp
35 40 45
Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
50 55 60
Pro Asp Ala Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro
65 70 75 80
Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg
85 90 95

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Arg Arg Trp Lys Ala Ala Ala Leu Val Ser Leu Ile Cys Ser Ser
1 5 10 15
Leu Leu Ser Val Trp Met Cys Gln Glu Gly Leu Leu Leu Gly His Arg
20 25 30
Leu Gly Pro Ala Leu Ala Pro Leu Arg Arg Pro Pro Arg Thr Leu Asp
35 40 45
Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
50 55 60
Pro Asp Ala Val Glu Leu Arg Glu Leu Ser Pro Trp Ala Ala Arg Ile
65 70 75 80
Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg
85 90 95

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

ATGCAGCGCT GGAAGGCGGC GGCCTTGGCC TCAGTGCTCT GCAGCTCCGT GCTGTCCATC      60
TGGATGTGTC GAGAGGGCCT GCTTCTCAGC CACCGCCTCG GACCTGCGCT GGTCCCCCTG      120
CACCGCCTGC CTCGAACCCT GGACGCCCCG ATTGCCCGCC TGGCCCAGTA CCGTGCACTC      180
CTGCAGGGGG CCCC GGATGC GATGGAGCTG CGCGAGCTGA CGCCCTGGGC TGGGCGGCCC      240
CCAGGTCCGC GCCGTCGGGC GGGGCCCCGG CGGCGGCGCG CGCGT                      285

```

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

ATGAGGCGCT GGAAGGCAGC GGCCCTGGTG TCGCTCATCT GCAGCTCCCT GCTATCTGTC      60
TGGATGTGCC AGGAGGGTCT GCTCTTGAGC CACCGCCTGG GACCCGCGCT TGCCCCGCTA      120
CGACGCCCTC CACGCACCCT GGACGCCCCG ATCGCCCGCC TGGCCCAGTA TCGCGCTCTG      180
CTCCAGGGCG CCCCCGACGC GGTGGAGCTT CGAGAACTTT CTCCCTGGGC TGCCCGCATC      240
CCGGGACCGC GCCGTCGAGC GGGTCCCCGG CGTCGGCGGG CGCGG                      285

```

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 169 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

ATGCAGCGCT GGAAGGCGGC GGCCTTGGCC TCAGTGCTCT GCAGCTCCGT GCTGTCCATC      60
TGGATGTGTC GAGAGGGCCT GCTTCTCAGC CACCGCCTCG GACCTGCGCT GGTCCCCCTG      120

```

CACCGCCTGC CTCGAACCTT GGACGCCCGG ATTGCCCGCC TGGCCCAGT

169

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 425 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ACCGTGCACT CCTGCAGGGG GCCCCGGATG CGATGGAGCT GCGCGAGCTG ACGCCCTGGG	60
CTGGGCGGCC CCCAGGTCCG CGCCGTCGGG CGGGGCCCG GCGGCGGCGC GCGCGTGCGC	120
GGTTGGGGGC GCGGCCTTGC GGGCTGCGCG AGCTGGAGGT GCGCGTGAGC GAGCTGGGCC	180
TGGGCTACGC GTCCGACGAG ACGGTGCTGT TCCGCTACTG CGCAGGCGCC TGCAGGCTG	240
CCGCGCGCGT CTACGACCTC GGGCTGCGAC GACTGCGCCA GCGGCGGCGC CTGCGGCGGG	300
AGCGGGTGCG CGCGCAGCCC TGCTGCCGCC CGACGGCCTA CGAGGACGAG GTGTCCTTCC	360
TGGACGCGCA CAGCCGCTAC CACACGGTGC ACGAGCTGTC GCGCGCGAG TGCCTGCG	420
TGTGA	425

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATGAGGCGCT GGAAGGCAGC GGCCCTGGTG TGCTCATCT GCAGCTCCCT GCTATCTGTC	60
TGGATGTGCC AGGAGGGTCT GCTCTTGGGC CACCGCCTGG GACCCGCGCT TGCCCCGCTA	120
CGACGCCCTC CACGCACCCT GGACGCCCGC ATCGCCCGCC TGGCCCAGT	169

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 419 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATCGCGCTCT GCTCCAGGGC GCGCCGACG CGGTGGAGCT TCGAGAACTT TCTCCCTGGG 60
 CTGCCCCGAT CCCGGGACCG CGCCGTCGAG CGGGTCCCCG GCGTCGGCGG GCGCGGCCGG 120
 GGGCTCGGCC TTGTGGGCTG CGCGAGCTCG AGGTGCGCGT GAGCGAGCTG GGCCTGGGCT 180
 ACACGTCGGA TGAGACCGTG CTGTTCCGCT ACTGCGCAGG CGCGTGCAGG GCGGCCATCC 240
 GCATCTACGA CCTGGGCCTT CGGCGCCTGC GCCAGCGGAG GCGCGTGCAG AGAGAGCGGG 300
 CGCGGGCGCA CCCGTGTTGT CGCCCGACGG CCTATGAGGA CGAGGTGTCC TTCCTGGACG 360
 TGCACAGCCG CTACCACACG CTGCAAGAGC TGTCGGCGCG GGAGTGCAGG TGCCTGTGA 419

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu Leu Gly Leu Gly
 1 5 10 15
 Tyr Ala Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys Ala Gly Ala Cys
 20 25 30
 Glu Ala Ala Ala Arg Val Tyr Asp Leu Gly Leu Arg Arg Leu Arg Gln
 35 40 45
 Arg Arg Arg Leu Arg Arg Glu Arg Val Arg Ala Gln Pro Cys Cys Arg
 50 55 60
 Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Ala His Ser Arg
 65 70 75 80
 Tyr His Thr Val His Glu Leu Ser Ala Arg Glu Cys Ala Cys
 85 90

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu Leu Gly Leu Gly
 1 5 10 15

Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys Ala Gly Ala Cys
 20 25 30
 Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu Arg Arg Leu Arg Gln
 35 40 45
 Arg Arg Arg Val Arg Arg Glu Arg Ala Arg Ala His Pro Cys Cys Arg
 50 55 60
 Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Val His Ser Arg
 65 70 75 80
 Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu Cys Ala Cys
 85 90

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "SERINE OR THREONINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC

ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Val Xaa Xaa Leu Gly Leu Gly Tyr
 1 5

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "THREONINE OR GLUTAMIC ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "LEUCINE OR ISOLEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC

ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 14
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Glu Xaa Xaa Xaa Phe Arg Tyr Cys Xaa Gly Xaa Cys Xaa Xaa Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "THREONINE OR VALINE OR

ISOLEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC

ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC

ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

- (B) LOCATION: 11
 (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Cys Cys Arg Pro Xaa Ala Xaa Xaa Asp Xaa Xaa Ser Phe Leu Asp
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 7
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 9
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC

ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 10
 (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Phe Arg Tyr Cys Xaa Gly Xaa Cys Xaa Xaa Ala
 1 5 10

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 7

(D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 9

(D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 10

(D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Phe Arg Tyr Cys Xaa Gly Xaa Cys Xaa Xaa Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 5

(D) OTHER INFORMATION: /note= "ISOLEUCINE OR THREONINE OR VALINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 7

(D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 8

(D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 10

(D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Cys Cys Arg Pro Xaa Ala Xaa Xaa Asp Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC

ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC

ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ala Xaa Xaa Asp Xaa Xaa Ser Phe Leu Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR THREONINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "LEUCINE OR VALINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "ISOLEUCINE OR LEUCINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Glu Xaa Xaa Xaa Phe Arg Tyr Cys
1 5

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR THREONINE"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /note= "LEUCINE OR VALINE"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 4
 (D) OTHER INFORMATION: /note= "ISOLEUCINE OR LEUCINE"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 9
 (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 13
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Glu Xaa Xaa Xaa Phe Arg Tyr Cys Xaa Gly Xaa Cys Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTNWSNGANY TNGGNYTNGG NTA

23

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TTYMGNTAYT GYDSNGGND S NTGYGANKCN GC

32

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GCNGMNTCRC ANSHNCCNSH RCARTANCKR AA

32

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCRTCNTCRW ANGCRYNGG NCKRCARCA

29

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TCNARRAANS WNAVNTCRTC NTCRWANGC

29

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GARRMNBTNH TNTTYMGNTA YTG

23

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GARRMNBTNH TNTTYMGNTA YTGYSNGGN DSNTGHGA

38

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1023 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGAGGGAGAG CGCGCGGTGG TTTCGTCCGT GTGCCCCGCG CCCGGCGCTC CTCGCGTGGC	60
CCCGCGTCCT GAGCGCGCTC CAGCCTCCCA CGCGCGCCAC CCCGGGGTTC ACTGAGCCCC	120
GCGAGCCCGG GGAAGACAGA GAAAGAGAGG CCAGGGGGGG AACCCCATGG CCCGGCCCCGT	180
GTCCCGCACC CTGTGCGGTG GCCTCCTCCG GCACGGGGTC CCCGGGTCGC CTCCGGTCCC	240
CGCGATCCGG ATGGCGCACG CAGTGGCTGG GGCCGGGCCG GGCTCGGGTG GTCGGAGGAG	300
TCACCACTGA CCGGGTCATC TGGAGCCCGT GGCAGGCGA GGCCAGGAT GAGGCGCTGG	360
AAGGCAGCGG CCCTGGTGTC GTCATCTGC AGCTCCCTGC TATCTGTCTG GATGTGCCAG	420
GAGGGTCTGC TCTTGGGCCA CCGCCTGGGA CCCGCGCTTG CCCCCTACG ACGCCCTCCA	480
CGCACCTTGG ACGCCCGCAT CGCCCGCCTG GCCAGTATC GCGCTCTGCT CCAGGGCGCC	540
CCCGACGCGG TGGAGCTTCG AGAACTTCT CCCTGGGCTG CCCGCATCCC GGGACCGCGC	600
CGTCGAGCGG GTCCCCGGCG TCGGCGGGCG CGGCCGGGGG CTCGGCCTTG TGGGCTGCGC	660
GAGCTCGAGG TGCGCGTGAG CGAGCTGGGC CTGGGCTACA CGTCGGATGA GACCGTGCTG	720
TTCCGCTACT GCGCAGGCGC GTGCGAGGCG GCCATCCGCA TCTACGACCT GGGCCTTCGG	780

CGCCTGCGCC AGCGGAGGCG CGTGCGCAGA GAGCGGGCGC GGGCGCACCC GTGTTGTCGC 840
 CCGACGGCCT ATGAGGACGA GGTGTCTTTC CTGGACGTGC ACAGCCGCTA CCACACGCTG 900
 CAAGAGCTGT CGGCGCGGGA GTGCGCGTGC GTGTGATGCT ACCTCACGCC CCCCACCTG 960
 CGAAAGGGCC CTCCTGCCG ACCCTCGCTG AGAACTGACT TCACATAAAG TGTGGGAACT 1020
 CCC 1023

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CCNACNGCNT AYGARGA

17

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly
 1 5 10 15
 Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys
 20 25 30
 Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg
 35 40 45
 Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro
 50 55 60
 Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr
 65 70 75 80
 His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys
 85 90

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ARYTCYTGNA RNGTRTGRTA

20

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GACGAGGTGT CCTTCTGGA CGTACACA

28

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TAGCGGCTGT GTACGTCCAG GAAGGACACC TCGT

34

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CAGCGACGAC GCGTGCGCAA AGAGCG

26

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TAYGARGACG AGGTGTCCTT CCTGGACGTA CACAGCCGCT AYCAAYAC

47

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GCGGCCATCC GCATCTACGA CCTGGG

26

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CRTAGGCCGT CGGGCGRCAR CACGGGT

27

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCGCCGAAGG CCCAGGTCGT AGATGCG

27

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CGCTACTGCG CAGGCGCGTG CGARGCGGC

29

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CGCCGACAGC TCTTGCAGCG TRTGGA

27

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GAGCTGGGCC TGGGCTACGC GTCCGACGAG

30

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCGACGCGTA CCATGAGGCG CTGGAAGGCA GCGGCCCTG

39

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GACGGATCCG CATCACACGC ACGCGCACTC

30

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GACCATATGC CGGGGGCTCG GCCTTGTTG

29

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GACGGATCCG CATCACACGC ACGCGCACTC

30

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CAGCGACGAC GCGTGCGCAA AGAGCG

26

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TAGCGGCTGT GTACGTCCAG GAAGGACACC TCGT

34

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

AAAAATCGGG GGTGYGTCTT A

21

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CATGCCTGGC CTACYTTGTC A

21

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CTGGCGTCCC AMCAAGGGTC TTCG

24

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GCCAGTGGTG CCGTCGAGGC GGG

23

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GGCCCAGGAT GAGGCCCTGG AAGG

24

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CCACTCCACT GCCTGAWATT CWACCCC

27

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCATGTGATT ATCGACCATT CGGC

24

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ser Pro Asp Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg
 1 5 10 15

Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg
 20 25 30
 Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu
 35 40 45
 Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile
 50 55 60
 Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp
 65 70 75 80
 Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys
 85 90 95
 Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser
 100 105 110
 Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala
 115 120 125
 Lys Arg Cys Gly Cys Ile
 130

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 134 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Ser Pro Asp Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Arg
 1 5 10 15
 Gln Ala Ala Ala Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg
 20 25 30
 Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu
 35 40 45
 Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile
 50 55 60
 Phe Arg Tyr Cys Ser Gly Ser Cys Glu Ser Ala Glu Thr Met Tyr Asp
 65 70 75 80
 Lys Ile Leu Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp Lys
 85 90 95
 Val Gly Gln Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser
 100 105 110
 Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala
 115 120 125
 Lys Arg Cys Gly Cys Ile
 130

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Ser Pro Asp Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Arg
 1 5 10 15

Gln Ala Ala Ala Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg
 20 25 30

Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu
 35 40 45

Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile
 50 55 60

Phe Arg Tyr Cys Ser Gly Ser Cys Glu Ala Ala Glu Thr Met Tyr Asp
 65 70 75 80

Lys Ile Leu Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp Lys
 85 90 95

Val Gly Gln Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser
 100 105 110

Phe Leu Asp Asp Ser Leu Val Tyr His Ile Leu Arg Lys His Ser Ala
 115 120 125

Lys Arg Cys Gly Cys Ile
 130

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu Gly
 1 5 10 15

Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser Cys
 20 25 30

Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg
 35 40 45

Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr
 50 55 60

Ala Asp Val Thr Phe Leu Asp Asp Gln His His Trp Gln Gln Leu Pro
 65 70 75 80
 Gln Leu Ser Ala Ala Ala Cys Gly Cys
 85

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Ala Leu Ala Gly Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala
 1 5 10 15
 Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr
 20 25 30
 Cys Ala Gly Ser Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val
 35 40 45
 Leu Ala Arg Leu Arg Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys
 50 55 60
 Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp Gln His His
 65 70 75 80
 Trp Gln Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 85 90 95

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

This sequence is intentionally skipped.

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu Gly
 1 5 10 15
 Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser Cys
 20 25 30
 Pro Gln Glu Val Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg
 35 40 45
 Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr
 50 55 60
 Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu Pro
 65 70 75 80
 Gln Leu Ser Ala Ala Ala Cys Gly Cys
 85

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu Gly
 1 5 10 15
 Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser Cys
 20 25 30
 Pro Gln Glu Val Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg
 35 40 45
 Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr
 50 55 60
 Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu Pro
 65 70 75 80
 Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 85 90

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TGCCGACTGT GGAGCCTGAC CCTACCACTG GCTGAGCTGG GCCTGGGCTA TGCCTCGGAG	60
GAGAAGGTCA TCTTCCGATA CTGTGCTGGC AGCTGTCCCC AAGAGGCCCG TACCCAGCAC	120
AGTCTGGTAC TGGCCCGCT TCGAGGGCGG GGTCGAGCCC ATGGCCGACC CTGCTGCCAG	180
CCCACCAGCT ATGCTGATGT GACCTTCCTT GATGATCAGC ACCATTGGCA GCAGCTGCCT	240
CAGCTCTCAG CTGCAGCTTG TGGCTGT	267

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TGCCGGCTGT GGAGCCTGAC CCTACCACTG GCTGAGCTTG GCCTGGGCTA TGCCTCAGAG	60
GAGAAGATTA TCTTCCGATA CTGTGCTGGC AGCTGTCCCC AAGAGGTCCG TACCCAGCAC	120
AGTCTGGTGC TGGCCCGTCT TCGAGGGCAG GGTCGAGCTC ATGGCAGACC TTGCTGCCAG	180
CCCACCAGCT ATGCTGATGT GACCTTCCTT GATGACCACC ACCATTGGCA GCAGCTGCCT	240
CAGCTCTCAG CCGCAGCTTG TGGCTGT	267

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

TGCCGGCTGT GGAGCCTGAC CCTACCACTG GCTGAGCTTG GCCTGGGCTA TGCCTCAGAG	60
GAGAAGATTA TCTTCCGATA CTGTGCTGGC AGCTGTCCCC AAGAGGTCCG TACCCAGCAC	120
AGTCTGGTGC TGGCCCGTCT TCGAGGGCAG GGTCGAGCTC ATGGCAGACC TTGCTGCCAG	180
CCCACCAGCT ATGCTGATGT GACCTTCCTT GATGACCACC ACCATTGGCA GCAGCTGCCT	240
CAGCTCTCAG CCGCAGCTTG TGGCTGTGGT GGC	273

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly
 1 5 10 15
 Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys
 20 25 30
 Glu Ser Ala Glu Thr Met Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg
 35 40 45
 Ser Arg Arg Leu Thr Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro
 50 55 60
 Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr
 65 70 75 80
 His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys Ile
 85 90

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu Leu Gly Leu Gly
 1 5 10 15
 Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys Ala Gly Ala Cys
 20 25 30
 Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu Arg Arg Leu Arg Gln
 35 40 45
 Arg Arg Arg Val Arg Arg Glu Arg Ala Arg Ala His Pro Cys Cys Arg
 50 55 60
 Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Val His Ser Arg
 65 70 75 80
 Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu Cys Ala Cys Val
 85 90 95

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 91 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu Gly
 1 5 10 15
 Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser Cys
 20 25 30
 Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg
 35 40 45
 Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr
 50 55 60
 Ala Asp Val Thr Phe Leu Asp Asp Gln His His Trp Gln Gln Leu Pro
 65 70 75 80
 Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 85 90

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TGCCTCAGAG GAGAAGATTA TC

22

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Ala Ser Glu Glu Lys Ile Ile
1 5

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AGTCGGGGTT GGGGTATGCC TCA

23

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TATGCCTCAG AGGAGAAGAT TATCTT

26

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CCTCAGAGGA GAAGATTATC TTCCGATACT GTGCTGGCAG CTGTCCCCAA GAGGTCCGTA	60
CCCAGCACAG TCTGGTGCTG GCCCGTCTTC GAGGGCAGGG TCGAGCTCAT GGCAGACCTT	120
GCTGCCAGCC CACCAGCTAT GCTGATGTGA CCTTCCTTGA TGACCACCAC CATTGGCAGC	180
AGCTGCCTCA GCTCTCAGCC GCAGCTTGTT GCTGTGGTGG CTGAAGGCGG CCAGCCTGGT	240
CTCTCAGAAT CACAAGCAAG AGGCAGCCTT TGAAAGGCTC AGGTGACGTT ATTAGAAACT	300
TGCATAGGAG AAGATTAAGA AGAGAAAGGG GACCTG	336

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
 1 5 10 15

Asp

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Lys Asp
 1 5 10 15

Val

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Pro Cys Cys Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCATCAAGGA AGGTCACATC AGCATA

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CCACCACAGC CACAAGCTGC GGSTGAGAGC TG

32

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Ala Leu Ala Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

This sequence is intentionally skipped

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 544 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GAGGGACCTG. GACGCCCCAT CAGGGTAAGA ATTCCTGGGG GCCTCCCGAC TCCCCAATTC 60
 CTTCTCTCAA AGCCCTCACT TTGCCTTACA ATCCTACTCT ACCTTGCACT AGGTAACAAC 120
 CATGTCCGTC TTCCAAGAGC CTTGGCTGGT TCATGCCGAC TGTGGAGCCT GACCCTACCA 180
 GTGGCTGAGC TGGGCTGGG CTATGCCTCG GAGGAGAAGG TCATCTCCG ATACTGTGCT 240
 GGCAGCTGTC CCCAAGAGGC CCGTACCCAG CACAGTCTGG TACTGGCCCG GCTTCGAGGG 300
 CGGGGTCGAG CCCATGGCCG ACCCTGCTGC CAGCCCACCA GCTATGCTGA TGTGACCTTC 360
 CTTGATGATC AGCACCATTG GCAGCAGCTG CCTCAGCTCT CAGCTGCAGC TTGTGGCTGT 420
 GGTGGCTGAA GGAGGCCAGT CTGGTGTCTC AGAATCACAA GCATGAGACA GGCTGGGCTT 480
 TGAAAGGCTC AGGTGACATT ACTAGAAATT TGCATAGGTA AAGATAAGAA GGGAAAGGAC 540
 CAGG 544

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser Cys Pro Gln
 1 5 10 15
 Glu Val Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg Gly Gln
 20 25 30
 Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr Ala Asp
 35 40 45
 Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu Pro Gln Leu
 50 55 60
 Ser Ala Ala Ala Cys Gly Cys Gly Gly
 65 70

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TGCCGGCTGT GGAGCCTGAC CCTACCACTG GCTGAGCTTG GCCTGGGCTA TGCCTCAGAG 60
 GAGAAGATTA TCTTCCGATA CTGTGCTGGC AGCTGTCCCC AAGAGGTCCG TACCCAGCAC 120
 AGTCTGGTGC TGGCCCGTCT TCGAGGGCAG GGTCGAGCTC ATGGCAGACC TTGCTGCCAG 180
 CCCACCAGCT ATGCTGATGT GACCTTCCTT GATGACCACC ACCATTGGCA GCAGCTGCCT 240
 CAGCTCTCAG CGGCAGCTTG TGGCTGTGGT GGCTGAAGGC GGCCAGCCTG GTCTCTCAGA 300
 ATCACAAGCA AGAGGCAGCC TTTGAAAGGC TCAGGTGACG TTATTAGAAA CTTGCATAGG 360
 AGAAGATTAA GAAGAGAAAG GGGACCTGAT T 391

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "SERINE, THREONINE, OR

ALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC

ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Val Xaa Xaa Leu Gly Leu Gly Tyr
 1 5

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Phe Arg Tyr Cys Xaa Gly Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /note= "ASPARTIC ACID, GLUTAMIC ACID OR NO AMINO ACID"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 3
(D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 4
(D) OTHER INFORMATION: /note= "SERINE OR THREONINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 8
(D) OTHER INFORMATION: /note= "valine or aspartic acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Asp Xaa Xaa Xaa Phe Leu Asp Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Glu Gly Pro Gly Arg Pro Ile Arg Val Arg Ile Pro Gly Gly Leu Pro
1 5 10 15

Thr Pro Gln Phe Leu Leu Ser Lys Pro Ser Leu Cys Leu Thr Ile Leu
20 25 30

Leu Tyr Leu Ala Leu Gly Asn Asn His Val Arg Leu Pro Arg Ala Leu
35 40 45

Ala Gly Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu
 50 55 60

Gly Leu Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala
 65 70 75 80

Gly Ser Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val Leu Ala
 85 90 95

Arg Leu Arg Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro
 100 105 110

Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp Gln His His Trp Gln
 115 120 125

Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 130 135 140

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Ala Leu Pro Gly Leu
 1 5

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "THREONINE, GLUTAMIC ACID OR
 LYSINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /note= "VALINE, LEUCINE OR
 ISOLEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 4
 (D) OTHER INFORMATION: /note= "LEUCINE OR ISOLEUCINE"

(ix) FEATURE:

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

Glu Xaa Xaa Xaa Phe Arg Tyr Cys Xaa Gly Xaa Cys
1 5 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /note= "ARGININE OR GLUTAMINE"

ISOLEUCINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 6
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 8
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID, ASPARTIC ACID OR ALANINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 10
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID, ASPARTIC ACID OR NO AMINO ACID"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site

- (B) LOCATION: 12
- (D) OTHER INFORMATION: /note= "SERINE OR THREONINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /note= "ASPARTIC ACID OR VALINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Cys Cys Xaa Pro Xaa Xaa Xaa Asp Xaa Xaa Xaa Phe Leu Asp Xaa
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GTNDGNGANY TGGGNYTGGG NTA

23

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GANBTNWCNT TYYTNGANG

19

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GANBTNWCNT TYYTNGANGW

20

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

TTYMGNTAYT GYDSNCGNDS NTG

23

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GTNDGNGANY TGGGNYTNGG

20

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GTNDGNGANY TGGGNYTGGG NTT

23

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

WCNTCNARRA ANGWNAVNTC

20

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

WCNTCNARRA ANGWNAVNT

19

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CANSHNCCNS HRCARTANCK RAA

23

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CANSHNCCNS HRCARTANCK RAANA

25

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

(B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "THREONINE, SERINE OR
 ALANINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 3

(D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC
 ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Val Xaa Xaa Leu Gly Leu Gly Tyr
 1 5

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 1

(D) OTHER INFORMATION: /note= "ASPARTIC ACID OR GLUTAMIC
 ACID"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 2

(D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 3

(D) OTHER INFORMATION: /note= "THREONINE OR SERINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 6

(D) OTHER INFORMATION: /note= "ASPARTIC ACID OR GLUTAMIC
 ACID"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 7

(D) OTHER INFORMATION: /note= "ASPARTIC ACID OR VALINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Xaa Xaa Xaa Phe Leu Xaa Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Phe Arg Tyr Cys Xaa Gly Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "THREONINE, SERINE OR ALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "ASPARTIC ACID OR GLUTAMIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Val Xaa Xaa Leu Gly Leu Gly
1 5

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "THREONINE, SERINE OR ALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Val Xaa Xaa Leu Gly Leu Gly Phe
1 5

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "ISOLEUCINE OR LEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Xaa Phe Arg Tyr Cys Xaa Gly Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

ATGGCTGCAG GAAGACTTCG GATCCTGTGT CTGCTGCTCC TGTCTTGCA CCCGAGCCTC	60
GGCTGGGTCC TTGATCTTCA AGAGGCTTCT GTGGCAGATA AGCTCTCATT TGGGAAGATG	120
GCAGAGACTA GAGGGACCTG GACGCCCCAT CAGGGTAAGA ATTCCTGGGG GCCTCCCGAC	180

TCCCCAATTC CTTCTCTCAA AGCCCTCACT TTGCCTTACA ATCCTACTCT ACCTTGCACT 240
 AGGTAACAAC CATGTCCGTC TTCCAAGAGC CTTGGCTGGT TCATGCCGAC TGTGGAGCCT 300
 GACCCTACCA GTGGCTGAGC TGGGCCTGGG CTATGCCTCG GAGGAGAAGG TCATCTTCCG 360
 ATACTGTGCT GGCAGCTGTC CCCAAGAGGC CCGTACCCAG CACAGTCTGG TACTGGCCCG 420
 GCTTCGAGGG CGGGGTCGAG CCCATGGCCG ACCCTGCTGC CAGCCACCA GCTATGCTGA 480
 TGTGACCTTC CTTGATGATC AGCACCATTG GCAGCAGCTG CCTCAGCTCT CAGCTGCAGC 540
 TTGTGGCTGT GCTGGCTGA 559

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 133 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Pro Asp Ala Arg Gly Val Pro Val Ala Asp Gly Glu Phe Ser Ser Glu
 1 5 10 15
 Gln Val Ala Lys Ala Gly Gly Thr Trp Leu Gly Thr His Arg Pro Leu
 20 25 30
 Ala Arg Leu Arg Arg Ala Leu Ser Gly Pro Cys Gln Leu Trp Ser Leu
 35 40 45
 Thr Leu Ser Val Ala Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys
 50 55 60
 Val Ile Phe Arg Tyr Cys Ala Gly Ser Cys Pro Arg Gly Ala Arg Thr
 65 70 75 80
 Gln His Gly Leu Ala Leu Ala Arg Leu Gln Gly Gln Gly Arg Ala His
 85 90 95
 Gly Gly Pro Cys Cys Arg Pro Thr Arg Tyr Thr Asp Val Ala Phe Leu
 100 105 110
 Asp Asp Arg His Arg Trp Gln Arg Leu Pro Gln Leu Ser Ala Ala Ala
 115 120 125
 Cys Gly Cys Gly Gly
 130

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

This sequence is intentionally skipped

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu	Gly
1				5					10					15	
Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys
			20					25					30		
Glu	Ala	Ala	Glu	Thr	Met	Tyr	Asp	Lys	Ile	Leu	Lys	Asn	Leu	Ser	Arg
			35				40					45			
Ser	Arg	Arg	Leu	Thr	Ser	Asp	Lys	Val	Gly	Gln	Ala	Cys	Cys	Arg	Pro
			50			55					60				
Val	Ala	Phe	Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp	Asp	Ser	Leu	Val	Tyr
65						70				75				80	
His	Ile	Leu	Arg	Lys	His	Ser	Ala	Lys	Arg	Cys	Gly	Cys			
				85					90						

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Met	Ala	Ala	Gly	Arg	Leu	Arg	Ile	Leu	Cys	Leu	Leu	Leu	Ser	Leu
1					5				10				15	
His	Pro	Ser	Leu	Gly	Trp	Val								
				20										

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met Ala Ala Gly Arg Leu Arg Ile Leu Phe Leu Leu Leu Ser Leu
1 5 10 15
His Leu Gly Leu Gly Trp Val
20

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

AATCCCCAGG ACAGGCAGGG AAT

23

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CGGTACCCAG ATCTTCAGCC ACCACAGCCA CAAGC

35

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGACTATCAT ATGGCCCACC ACCACCACCA CCACCACCAC GACGACGACG ACAAGGCCTT

60

GGCTGGTTCA TGCCGA

76

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

TGCTGTCACC ATGGCTGCAG GAAGACTTCG GA

32

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Ala	Leu	Ala	Gly	Ser	Cys	Arg	Leu	Trp	Ser	Leu	Thr	Leu	Pro	Val	Ala	1	5	10	15
Glu	Leu	Gly	Leu	Gly	Tyr	Ala	Ser	Glu	Glu	Lys	Val	Ile	Phe	Arg	Tyr	20	25	30	
Cys	Ala	Gly	Ser	Cys	Pro	Gln	Glu	Ala	Arg	Thr	Gln	His	Ser	Leu	Val	35	40	45	
Leu	Ala	Arg	Leu	Arg	Gly	Arg	Gly	Arg	Ala	His	Gly	Arg	Pro	Cys	Cys	50	55	60	
Arg	Pro	Thr	Ala	Tyr	Glu	Asp	Glu	Val	Ser	Phe	Leu	Asp	Val	His	Ser	65	70	75	80
Arg	Tyr	His	Thr	Leu	Gln	Glu	Leu	Ser	Ala	Arg	Glu	Cys	Ala	Cys	Val	85	90	95	

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TAATACGACT CACTATAGGG GAA

23

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

TCGTCTTCGT AAGCAGTCGG ACGGCAGCAG GGTCCGCCAT GGGCTCGAC

49

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TGCTGCCGTC CGACTGCTTA CGAGACGA

29

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GTTATGCTAG TTATTGCTCA GCGGT

25

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Pro Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser
 1 5 10 15
 Glu Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr
 20 25 30
 Cys Ala Gly Ala Cys Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu
 35 40 45
 Arg Arg Leu Arg Gln Arg Arg Arg Val Arg Arg Glu Arg Ala Arg Ala
 50 55 60
 His Pro Cys Cys Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp
 65 70 75 80
 Asp Gln His His Trp Gln Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys
 85 90 95
 Gly Cys Gly Gly
 100

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CACATCAGCA TAGCTGGTGG GCTGGCAGCA CGGGTGAGCA CGAGCACGTT

50

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TGCTGCCAGC CCACCAGCTA TGCTG

25

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CCTCGGAGGA GAAGGTCATC TTC

23

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Cys	Cys	Val	Arg	Gln	Leu	Tyr	Ile	Asp	Phe	Arg	Lys	Asp	Leu	Gly	Trp
1				5					10					15	
Lys	Trp	Ile	His	Glu	Pro	Lys	Gly	Tyr	His	Ala	Asn	Phe	Cys	Leu	Gly
		20						25					30		
Pro	Cys	Pro	Tyr	Ile	Trp	Ser	Leu	Asp	Thr	Gln	Tyr	Ser	Lys	Val	Leu
		35					40					45			
Ala	Leu	Tyr	Asn	Gln	His	Asn	Pro	Gly	Ala	Ser	Ala	Ala	Pro	Cys	Cys
	50					55					60				
Val	Pro	Gln	Ala	Leu	Glu	Pro	Leu	Pro	Ile	Val	Tyr	Tyr	Val	Gly	Arg
65				70					75					80	
Lys	Pro	Lys	Val	Glu	Gln	Leu	Ser	Asn	Met	Ile	Val	Arg	Ser	Cys	Lys
				85				90						95	
Cys	Ser														

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Cys	Cys	Leu	Arg	Pro	Leu	Tyr	Ile	Asp	Phe	Lys	Arg	Asp	Leu	Gly	Trp
1				5					10					15	

Lys Trp Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly
 20 25 30
 Ala Cys Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val Leu
 35 40 45
 Ser Leu Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys
 50 55 60
 Val Ser Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Lys
 65 70 75 80
 Thr Pro Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys
 85 90 95
 Cys Ser

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 98 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln Asp Leu Gly Trp
 1 5 10 15
 Lys Trp Val His Glu Pro Lys Gly Tyr Tyr Ala Asn Phe Cys Ser Gly
 20 25 30
 Pro Cys Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu
 35 40 45
 Gly Leu Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys
 50 55 60
 Val Pro Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg
 65 70 75 80
 Thr Pro Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys
 85 90 95
 Cys Ser

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Cys Cys Lys Lys Gln Phe Phe Val Ser Phe Lys Asp Ile Gly Trp Asn
 1 5 10 15
 Asp Trp Ile Ile Ala Pro Ser Gly Tyr His Ala Asn Tyr Cys Glu Gly
 20 25 30
 Glu Cys Pro Ser His Ile Ala Gly Thr Ser Gly Ser Ser Leu Ser Phe
 35 40 45
 His Ser Thr Val Ile Asn His Tyr Arg Met Arg Gly His Ser Pro Phe
 50 55 60
 Ala Asn Leu Lys Ser Cys Cys Val Pro Thr Lys Leu Arg Pro Met Ser
 65 70 75 80
 Met Leu Tyr Tyr Asp Asp Gly Gln Asn Ile Ile Lys Lys Asp Ile Gln
 85 90 95
 Asn Met Ile Val Glu Glu Cys Gly Cys Ser
 100 105

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Cys Cys Arg Gln Gln Phe Phe Ile Asp Phe Arg Leu Ile Gly Trp Asn
 1 5 10 15
 Asp Trp Ile Ile Ala Pro Thr Gly Tyr Tyr Gly Asn Tyr Cys Glu Gly
 20 25 30
 Ser Cys Pro Ala Tyr Leu Ala Gly Val Pro Gly Ser Ala Ser Ser Phe
 35 40 45
 His Thr Ala Val Val Asn Gln Tyr Arg Met Arg Gly Leu Asn Pro Gly
 50 55 60
 Thr Val Asn Ser Cys Cys Ile Pro Thr Lys Leu Ser Thr Met Ser Met
 65 70 75 80
 Leu Tyr Phe Asp Asp Glu Tyr Asn Ile Val Lys Arg Asp Val Pro Asn
 85 90 95
 Met Ile Val Glu Glu Cys Gly Cys Ala
 100 105

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Cys Arg Arg Val Lys Phe Gln Val Asp Phe Asn Leu Ile Gly Trp Gly
1 5 10 15
Ser Trp Ile Ile Tyr Pro Lys Gln Tyr Asn Ala Tyr Arg Cys Glu Gly
20 25 30
Glu Cys Pro Asn Pro Val Gly Glu Glu Phe His Pro Thr Asn His Ala
35 40 45
Tyr Ile Gln Ser Leu Leu Lys Arg Tyr Gln Pro His Arg Val Pro Ser
50 55 60
Thr Cys Cys Ala Pro Val Lys Thr Lys Pro Leu Ser Met Leu Tyr Val
65 70 75 80
Asp Asn Gly Arg Val Leu Leu Glu His His Lys Asp Met Ile Val Glu
85 90 95
Glu Cys Gly Cys Leu
100

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn
1 5 10 15
Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly
20 25 30
Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala
35 40 45
Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala
50 55 60
Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp
65 70 75 80
Glu Asn Glu Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu
85 90 95
Gly Cys Gly Cys Arg
100

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn
 1 5 10 15
 Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly
 20 25 30
 Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala
 35 40 45
 Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys Ala
 50 55 60
 Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp
 65 70 75 80
 Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val Glu
 85 90 95
 Gly Cys Gly Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asp
 1 5 10 15
 Asp Trp Ile Val Ala Pro Leu Gly Tyr Asp Ala Tyr Tyr Cys His Gly
 20 25 30
 Lys Cys Pro Phe Pro Leu Ala Asp His Phe Asn Ser Thr Asn His Ala
 35 40 45
 Val Val Gln Thr Leu Val Asn Asn Met Asn Pro Gly Lys Val Pro Lys
 50 55 60
 Ala Cys Cys Val Pro Thr Gln Leu Asp Ser Val Ala Met Leu Tyr Leu
 65 70 75 80

Asn Asp Gln Ser Thr Val Val Leu Lys Asn Tyr Gln Glu Met Thr Val
85 90 95

Val Gly Cys Gly Cys Arg
100

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln
1 5 10 15
Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly
20 25 30
Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
35 40 45
Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro Lys
50 55 60
Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
65 70 75 80
Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
85 90 95
Arg Ser Cys Gly Cys His
100

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Cys Arg Lys His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln
1 5 10 15
Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly
20 25 30
Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
35 40 45

Ile Val Gln Thr Leu Val His Leu Met Asn Pro Glu Tyr Val Pro Lys
 50 55 60
 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
 65 70 75 80
 Asp Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
 85 90 95
 Arg Ala Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln
 1 5 10 15
 Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly
 20 25 30
 Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala Thr Asn His Ala
 35 40 45
 Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Glu Thr Val Pro Lys
 50 55 60
 Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser Val Leu Tyr Phe
 65 70 75 80
 Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
 85 90 95
 Arg Ala Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu
 1 5 10 15

Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly
 20 25 30
 Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala
 35 40 45
 Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys
 50 55 60
 Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr
 65 70 75 80
 Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn Met Val Val
 85 90 95
 Lys Ala Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Cys Gln Met Gln Thr Leu Tyr Ile Asp Phe Lys Asp Leu Gly Trp His
 1 5 10 15
 Asp Trp Ile Ile Ala Pro Glu Gly Tyr Gly Ala Phe Tyr Cys Ser Gly
 20 25 30
 Glu Cys Asn Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
 35 40 45
 Ile Val Gln Thr Leu Val His Leu Leu Glu Pro Lys Lys Val Pro Lys
 50 55 60
 Pro Cys Cys Ala Pro Thr Arg Leu Gly Ala Leu Pro Val Leu Tyr His
 65 70 75 80
 Leu Asn Asp Glu Asn Val Asn Leu Lys Lys Tyr Arg Asn Met Ile Val
 85 90 95
 Lys Ser Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 103 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Cys Ala Arg Arg Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp Ser
 1 5 10 15
 Glu Trp Ile Ile Ser Pro Lys Ser Phe Asp Ala Tyr Tyr Cys Ser Gly
 20 25 30
 Ala Cys Gln Phe Pro Met Pro Lys Ser Leu Lys Pro Ser Asn His Ala
 35 40 45
 Thr Ile Gln Ser Ile Val Arg Ala Val Gly Val Val Pro Gly Ile Pro
 50 55 60
 Glu Pro Cys Cys Val Pro Glu Lys Met Ser Ser Leu Ser Ile Leu Phe
 65 70 75 80
 Phe Asp Glu Asn Lys Asn Val Val Leu Lys Val Tyr Pro Asn Met Thr
 85 90 95
 Val Glu Ser Cys Ala Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Cys Lys Lys Arg His Leu Tyr Val Glu Phe Lys Asp Val Gly Trp Gln
 1 5 10 15
 Asn Trp Val Ile Ala Pro Gln Gly Tyr Met Ala Asn Tyr Cys Tyr Gly
 20 25 30
 Glu Cys Pro Tyr Pro Leu Thr Glu Ile Leu Asn Gly Ser Asn His Ala
 35 40 45
 Ile Leu Gln Thr Leu Val His Ser Ile Glu Pro Glu Asp Ile Pro Leu
 50 55 60
 Pro Cys Cys Val Pro Thr Lys Met Ser Pro Ile Ser Met Leu Phe Tyr
 65 70 75 80
 Asp Asn Asn Asp Asn Val Val Leu Arg His Tyr Glu Asn Met Ala Val
 85 90 95
 Asp Glu Cys Gly Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Cys	Arg	Ala	Arg	Arg	Leu	Tyr	Val	Ser	Phe	Arg	Glu	Val	Gly	Trp	His
1				5					10					15	
Arg	Trp	Val	Ile	Ala	Pro	Arg	Gly	Phe	Leu	Ala	Asn	Tyr	Cys	Gln	Gly
		20					25						30		
Gln	Cys	Ala	Leu	Pro	Val	Ala	Leu	Ser	Gly	Ser	Gly	Gly	Pro	Pro	Ala
	35						40					45			
Leu	Asn	His	Ala	Val	Leu	Arg	Ala	Leu	Met	His	Ala	Ala	Ala	Pro	Gly
	50					55				60					
Ala	Ala	Asp	Leu	Pro	Cys	Cys	Val	Pro	Ala	Arg	Leu	Ser	Pro	Ile	Ser
65					70				75					80	
Val	Leu	Phe	Phe	Asp	Asn	Ser	Asp	Asn	Val	Val	Leu	Arg	Gln	Tyr	Glu
				85					90					95	
Asp	Met	Val	Val	Asp	Glu	Cys	Gly	Cys	Arg						
				100					105						

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Cys	His	Arg	His	Gln	Leu	Phe	Ile	Asn	Phe	Gln	Asp	Leu	Gly	Trp	His
1				5					10					15	
Lys	Trp	Val	Ile	Ala	Pro	Lys	Gly	Phe	Met	Ala	Asn	Tyr	Cys	His	Gly
		20					25						30		
Glu	Cys	Pro	Phe	Ser	Met	Thr	Thr	Tyr	Leu	Asn	Ser	Ser	Asn	Tyr	Ala
	35						40					45			
Phe	Met	Gln	Ala	Leu	Met	His	Met	Ala	Asp	Pro	Lys	Val	Pro	Lys	Ala
	50					55					60				
Val	Cys	Val	Pro	Thr	Lys	Leu	Ser	Pro	Ile	Ser	Met	Leu	Tyr	Gln	Asp
65					70				75					80	
Ser	Asp	Lys	Asn	Val	Ile	Leu	Arg	His	Tyr	Glu	Asp	Met	Val	Val	Asp
			85						90					95	
Glu	Cys	Gly	Cys	Gly											
				100											

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Cys Arg Arg Thr Ser Leu His Val Asn Phe Lys Glu Ile Gly Trp Asp
 1 5 10 15
 Ser Trp Ile Ile Ala Pro Lys Asp Tyr Glu Ala Phe Glu Cys Lys Gly
 20 25 30
 Gly Cys Phe Phe Pro Leu Thr Asp Asn Val Thr Pro Thr Lys His Ala
 35 40 45
 Ile Val Gln Thr Leu Val His Leu Gln Asn Pro Lys Lys Ala Ser Lys
 50 55 60
 Ala Cys Cys Val Pro Thr Lys Leu Asp Ala Ile Ser Ile Leu Tyr Lys
 65 70 75 80
 Asp Asp Ala Gly Val Pro Thr Leu Ile Tyr Asn Tyr Glu Gly Met Lys
 85 90 95
 Val Ala Glu Cys Gly Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Cys His Arg Val Ala Leu Asn Ile Ser Phe Gln Glu Leu Gly Trp Glu
 1 5 10 15
 Arg Trp Ile Val Tyr Pro Pro Ser Phe Ile Phe His Tyr Cys His Gly
 20 25 30
 Gly Cys Gly Leu His Ile Pro Pro Asn Leu Ser Leu Pro Val Pro Gly
 35 40 45
 Ala Pro Pro Thr Pro Ala Gln Pro Tyr Ser Leu Leu Pro Gly Ala Gln
 50 55 60
 Pro Cys Cys Ala Ala Leu Pro Gly Thr Met Arg Pro Leu His Val Arg
 65 70 75 80

Thr Thr Ser Asp Gly Gly Tyr Ser Phe Lys Tyr Glu Thr Val Pro Asn
85 90 95

Leu Leu Thr Gln His Cys Ala Cys Ile
100 105

(2) INFORMATION FOR SEO ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

[illegible]

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Cys Glu Leu His Asp Phe Ser Leu Ser Phe Ser Gln Leu Lys Trp Asp
1 5 10 15
Asn Trp Ile Val Ala Pro His Ser Tyr Asn Pro Ser Tyr Cys Lys Gly
20 25 30
Asp Cys Pro Ser Ala Val Ser His Arg Tyr Gly Ser Pro Val His Thr
35 40 45

Met Val Gln Asn Met Ile Tyr Glu Lys Leu Asp Pro Ser Val Pro Ser
 50 55 60
 Pro Ser Cys Val Pro Gly Lys Tyr Ser Pro Leu Ser Val Leu Thr Ile
 65 70 75 80
 Glu Pro Asp Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp Met Met Ala
 85 90 95
 Thr Ser Cys Thr Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly
 1 5 10 15
 Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys
 20 25 30
 Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg
 35 40 45
 Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro
 50 55 60
 Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr
 65 70 75 80
 His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys Ile
 85 90

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu Leu Gly Leu Gly
 1 5 10 15
 Tyr Ala Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys Ala Gly Ala Cys
 20 25 30

Glu Ala Ala Ala Arg Val Tyr Asp Leu Gly Leu Arg Arg Leu Arg Gln
 35 40 45
 Arg Arg Arg Leu Arg Arg Glu Arg Val Arg Ala Gln Pro Cys Cys Arg
 50 55 60
 Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Ala His Ser Arg
 65 70 75 80
 Tyr His Thr Val His Glu Leu Ser Ala Arg Glu Cys Ala Cys Val
 85 90 95

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Leu Asp Leu Gln Glu Ala Ser Val Ala Asp Lys Leu Ser Phe Gly Lys
 1 5 10 15
 Met Ala Glu Thr Arg Gly Thr Trp Thr Pro His Gln Gly Asn Asn His
 20 25 30
 Val Arg Leu Pro Arg
 35

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Leu Asp Leu Gln Glu Ala Pro Ala Ala Asp Glu Leu Ser Ser Gly Lys
 1 5 10 15
 Met Ala Glu Thr Gly Arg Thr Trp Lys Pro His Gln Gly Asn Asn Asn
 20 25 30
 Val Arg Leu Pro Arg
 35

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly
1 5 10 15
Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys
20 25 30
Glu Ser Ala Glu Thr Met Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg
35 40 45
Ser Arg Arg Leu Thr Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro
50 55 60
Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr
65 70 75 80
His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys
85 90

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 723 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

ATGGCTGCAG GAAGACTTCG GATCCTGTGT CTGCTGCTCC TGTCTTGCA CCCGAGCCTC 60
GGCTGGGTCC TTGATCTTCA AGAGGCTTCT GTGGCAGATA AGCTCTCATT TGGGAAGATG 120
GCAGAGACTA GAGGGACCTG GACGCCCCAT CAGGGTAAGA ATTCCTGGGG GCCTCCCGAC 180
TCCCCAATTC CTTCTCTCAA AGCCCTCACT TTGCCTTACA ATCCTACTCT ACCTTGCACT 240
AGGTAACAAC CATGTCCGTC TTCCAAGAGC CTTGGCTGGT TCATGCCGAC TGTGGAGCCT 300
GACCCTACCA GTGGCTGAGC TGGGCCTGGG CTATGCCTCG GAGGAGAAGG TCATCTTCCG 360
ATACTGTGCT GGCAGCTGTC CCAAGAGGC CCGTACCCAG CACAGTCTGG TACTGGCCCCG 420
GCTTCGAGGG CGGGGTCGAG CCCATGGCCG ACCCTGCTGC CAGCCCACCA GCTATGCTGA 480
TGTGACCTTC CTTGATGATC AGCACCATTG GCAGCAGCTG CCTCAGCTCT CAGCTGCAGC 540
TTGTGGCTGT GGTGGCTGAA GGAGGCCAGT CTGGTGTCTC AGAATCACAA GCATGAGACA 600
GGCTGGGCTT TGAAAGGCTC AGGTGACATT ACTAGAAATT TGCATAGGTA AAGATAAGAA 660
GGGAAAGGAC CAGGGGTTTT TTGTTTCTTT CTTTGCTTGC TTGTTAGTTT TTTTTTTTTT 720

TTT

723

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 723 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

AAAAAAAAAA AAAA AACTAA CAAGCAAGCA AAGAAAGAAA CAAAAAACCC CTGGTCCTTT 60
 CCCTTCTTAT CTTTACCTAT GCAAATTTCT AGTAATGTCA CCTGAGCCTT TCAAAGCCCCA 120
 GCCTGTCTCA TGCTTGTGAT TCTGAGACAC CAGACTGGCC TCCTTCAGCC ACCACAGCCA 180
 CAAGCTGCAG CTGAGAGCTG AGGCAGCTGC TGCCAATGGT GCTGATCATC AAGGAAGGTC 240
 ACATCAGCAT AGCTGGTGGG CTGGCAGCAG GGTGCGCCAT GGGCTCGACC CCGCCCTCGA 300
 AGCCGGGCCA GTACCAGACT GTGCTGGGTA CGGGCCTCTT GGGGACAGCT GCCAGCACAG 360
 TATCGGAAGA TGACCTTCTC CTCCGAGGCA TAGCCCAGGC CCAGCTCAGC CACTGGTAGG 420
 GTCAGGCTCC ACAGTCGGCA TGAACCAGCC AAGGCTCTTG GAAGACGGAC ATGGTTGTTA 480
 CCTAGTGCAA GGTAAGTAG GATTGTAAGG CAAAGTGAGG GCTTTGAGAG AAGGAATTGG 540
 GGAGTCGGGA GGCCCCCAGG AATTCTTACC CTGATGGGGC GTCCAGGTCC CTCTAGTCTC 600
 TGCCATCTTC CCAAATGAGA GCTTATCTGG CACAGAAGCC TCTTGAAGAT CAAGGACCCA 660
 GCCGAGGCTC GGGTGCAAGG ACAGGACAG CAGACACAGG ATCCGAAGTC TTCCTGCAGC 720
 CAT 723

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

ATGGCTGCAG GAAGACTTCG GATCCTGTGT CTGCTGCTCC TGTCCTTGCA CCCGAGCCTC 60
 GGCTGGGTCC TTGATCTTCA AGAGGCTTCT GTGGCAGATA AGCTCTCATT TGGGAAGATG 120
 GCAGAGACTA GAGGGACCTG GACGCCCCAT CAGGGTAACA ACCATGTCCG TCTTCCAAGA 180
 GCCTTGGCTG GTTCATGCCG ACTGTGGAGC CTGACCCTAC CAGTGGCTGA GCTGGGCCTG 240

GGCTATGCCT CGGAGGAGAA GGTCACTTTC CGATACTGTG CTGGCAGCTG TCCCCAAGAG 300
 GCCCGTACCC AGCACAGTCT GGTACTGGCC CGGCTTCGAG GCGGGGGTCG AGCCCATGGC 360
 CGACCCTGCT GCCAGCCAC CAGCTATGCT GATGTGACCT TCCTTGATGA TCAGCACCAT 420
 TGGCAGCAGC TGCCTCAGCT CTCAGCTGCA GCTTGTGGCT GTGGTGGCTG A 471

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 471 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

TCAGCCACCA CAGCCACAAG CTGCAGCTGA GAGCTGAGGC AGCTGCTGCC AATGGTGCTG 60
 ATCATCAAGG AAGGTCACAT CAGCATAGCT GGTGGGCTGG CAGCAGGGTC GGCCATGGGC 120
 TCGACCCCGC CCTCGAAGCC GGGCCAGTAC CAGACTGTGC TGGGTACGGG CCTCTTGGGG 180
 ACAGCTGCCA GCACAGTATC GGAAGATGAC CTTCTCTCC GAGGCATAGC CCAGGCCCAG 240
 CTCAGCCACT GGTAGGGTCA GGCTCCACAG TCGGCATGAA CCAGCCAAGG CTCTTGAAG 300
 ACGGACATGG TTGTTACCCT GATGGGGCGT GCAGGTCCCT CTAGTCTCTG CCATCTTCCC 360
 AAATGAGAGC TTATCTGCCA CAGAAGCTCT TTGAAGATCA AGGACCCAGC CGAGGCTCGG 420
 GTGCAAGGAC AGGAGCAGCA GACACAGCAT CCGAAGTCTT CCTGCAGCCA T 471

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 180 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

ATGGCTGCAG GAAGACTTCG GATCCTGTGT CTGCTGCTCC TGTCTTGCA CCCGAGCCTC 60
 GGCTGGGTCC TTGATCTTCA AGAGGCTTCT GTGGCAGATA AGCTCTCATT TGGGAAGATG 120
 GCAGAGACTA GAGGGACCTG GACGCCCCAT CAGGGTAACA ACCATGTCCG TCTTCCAAGA 180

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 180 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TCTTGAAGA CGGACATGGT TGTTACCCTG ATGGGGCGTC CAGGTCCCTC TAGTCTCTGC	60
CATCTTCCCA AATGAGAGCT TATCTGCCAC AGAAGCCTCT TGAAGATCAA GGACCCAGCC	120
GAGGCTCGGG TGCAAGGACA GGAGCAGCAG ACACAGGATC CGAAGTCTTC CTGCAGCCAT	180

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GCCTTGGCTG GTTCATGCCG ACTGTGGAGC CTGACCCTAC CAGTGGCTGA GCTGGGCCTG	60
GGCTATGCCT CGGAGGAGAA GGTCATCTTC CGATACTGTG CTGGCAGCTG TCCCCAAGAG	120
GCCCGTACCC AGCACAGTCT GGTACTGGCC CGGCTTCGAG GGCGGGGTCG AGCCCATGGC	180
CGACCCTGCT GCCAGCCCAC CAGCTATGCT GATGTGACCT TCCTTGATGA TCAGCACCAT	240
TGGCAGCAGC TGCCTCAGCT CTCAGCTGCA GCTTGTGGCT GTGGTGGCTG A	291

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

TCAGCCACCA CAGCCACAAG CTGCAGCTGA GAGCTGAGGC AGCTGCTGCC AATGGTGCTG	60
ATCATCAAGG AAGGTCACAT CAGCATAGCT GGTGGGCTGG CAGCAGGGTC GGCCATGGGC	120
TGCACCCCGC CCTCGAAGCC GGGCCAGTAC CAGACTGTGC TGGGTACGGG CCTCTTGGGG	180
ACAGCTGCCA GCACAGTATC GGAAGATGAC CTTCTCCTCC GAGGCATAGC CCAGGCCAG	240
CTCAGCCACT GGTAGGTGCA GGCTCCACAG TCGGCATGAA CCAGCCAAGG C	291

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Met Ala Ala Gly Arg Leu Arg Ile Leu Cys Leu Leu Leu Ser Leu
 1 5 10 15
 His Pro Ser Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Ser Val Ala
 20 25 30
 Asp Lys Leu Ser Phe Gly Lys Met Ala Glu Thr Arg Gly Thr Trp Thr
 35 40 45
 Pro His Gln Gly Asn Asn His Val Arg Leu Pro Arg Ala Leu Ala Gly
 50 55 60
 Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu
 65 70 75 80
 Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser
 85 90 95
 Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu
 100 105 110
 Arg Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser
 115 120 125
 Tyr Ala Asp Val Thr Phe Leu Asp Asp Gln His His Trp Gln Gln Leu
 130 135 140
 Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 145 150 155

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Met Ala Ala Gly Arg Leu Arg Ile Leu Cys Leu Leu Leu Ser Leu
 1 5 10 15
 His Pro Ser Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Ser Val Ala
 20 25 30

Asp Lys Leu Ser Phe Gly Lys Met Ala Glu Thr Arg Gly Thr Trp Thr
 35 40 45
 Pro His Gln Gly Asn Asn His Val Arg Leu Pro Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Ala Leu Ala Gly Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala
 1 5 10 15
 Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr
 20 25 30
 Cys Ala Gly Ser Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val
 35 40 45
 Leu Ala Arg Leu Arg Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys
 50 55 60
 Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp Gln His His
 65 70 75 80
 Trp Gln Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 85 90 95

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

ATGGCTGCAG GAAGACTTCG GATCTTGTTC CTGCTGCTCC TGTCTTGCA CCTGGGCCTT 60
 GGCTGGGTCC TTGATCTTCA AGAGGCTCCT GCGGCAGATG AGCTCTCATC TGGGAAAATG 120
 GCAGAGACTG GAAGGACCTG GAAGCCCCAT CAGGTAAGA ATTCTTGGGG GCCTCCTAAC 180
 TCTACAGTTC TTCCTCTCAA AGCCCTCACT TTGCCTCACA ATCCTATTCT ACCTTGCACT 240
 AGGTAACAAC AATGTCCGCC TTCCAAGAGC CTTACCTGGT TTGTGCCGGC TGTGGAGCCT 300
 GACCCTACCA GTGGCTGAGC TTGGCCTGGG CTATGCCTCA GAGGAGAAGA TTATCTTCGG 360

ATACTGTGCT GGCAGCTGTC CCCAAGAGGT CCGTACCCAG CACAGTCTGG TGCTGGCCCCG 420
 TCTTCGAGGG CAGGGTCGAG CTCATGGCAG ACCTTGCTGC CAGCCCACCA GCTATGCTGA 480
 TGTGACCTTC CTTGATGACC ACCACCATTG GCAGCAGCTG CCTCAGCTCT CAGCCGCAGC 540
 TTGTGGCTGT GGTGGCTGA 559

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 559 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TCAGCCACCA CAGCCACAAG CTGCGGCTGA GAGCTGAGGC AGCTGCTGCC AATGGTGGTG 60
 GTCATCAAGG AAGGTCACAT CAGCATAGCT GGTGGGCTGG CAGCAAGGTC TGCCATGAGC 120
 TCGACCCTGC CCTCGAAGAC GGGCCAGCAC CAGACTGTGC TGGGTACGGA CCTCTTGGGG 180
 ACAGCTGCCA GCACAGTATC GGAAGATAAT CTTCTCCTCT GAGGCATAGC CCAGGCCAAG 240
 CTCAGCCACT GGTAGGGTCA GGTCCACAG CCGGCACAAA CCAGGTAAGG CTCTTGGAAG 300
 GCGGACATTG TTGTTACCTA CTGCAAGGTA GAATAGGATT GTGAGGCAAA GTGAGGGCTT 360
 TGAGAGGAAG AACTGTAGAG TTAGGAGGCC CCCAAGAATT CTTACCCTGA TGGGGCTTCC 420
 AGGTCCTTCC AGTCTCTGCC ATTTTCCCAG ATGAGAGCTC ATCTGCCGCA GGAGCCTCTT 480
 GAAGATCAAG GACCCAGCCA AGGCCAGGT GCAAGGACAG GAGCAGCAGA AACAAGATCC 540
 GAAGTCTTCC TGCAGCCAT 559

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

ATGGCTGCAG GAAGACTTCG GATCTGTTT CTGCTCTCC TGTCTTGCA CCTGGGCCTT 60
 GGCTGGGTCC TTGATCTTCA AGAGGCTCCT GCGGCAGATG AGCTCTCATC TGGGAAAATG 120
 GCAGAGACTG GAAGGACCTG GAAGCCCCAT CAGGGTAACA ACAATGTCCG CCTTCCAAGA 180
 GCCTTACCTG GTTGTGCCG GCTGTGGAGC CTGACCTAC CAGTGGCTGA GCTTGGCCTG 240

GGCTATGCCT CAGAGGAGAA GATTATCTTC CGATACTGTG CTGGCAGCTG TCCCCAAGAG 300
 GTCCGTACCC AGCACAGTCT GGTGCTGGCC CGTCTTCGAG GGCAGGGTCG AGCTCATGGC 360
 AGACCTTGCT GCCAGCCCAC CAGCTATGCT GATGTGACCT TCCTTGATGA CCACCACCAT 420
 TGGCAGCAGC TGCCTCAGCT CTCAGCCGCA GCTTGTGGCT GTGGTGGCTG A 471

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 471 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

TCAGCCACCA CAGCCACAAG CTGCGGCTGA GAGCTGAGGC AGCTGCTGCC AATGGTGGTG 60
 GTCATCAAGG AAGGTCACAT CAGCATAGCT GGTGGGCTGG CAGCAAGGTC TGCCATGAGC 120
 TCGACCCTGC CCTCGAAGAC GGGCCAGCAC CAGACTGTGC TGGGTACGGA CCTCTTGGGG 180
 ACAGCTGCCA GCACAGTATC GGAAGATAAT CTTCTCTCT GAGGCATAGC CCAGGCCAAG 240
 CTCAGCCACT GGTAGGGTCA GGCTCCACAG CCGGCACAAA CCAGGTAAGG CTCTTGGAAG 300
 GCGGACATTG TTGTTACCCT GATGGGGCTT CCAGGTCCTT CCAGTCTCTG CCATTTTCCC 360
 AGATGAGAGC TCATCTGCCG CAGGAGCCTC TTGAAGATCA AGGACCCAGC CAAGGCCCAG 420
 GTGCAAGGAC AGGAGCAGCA GAAACAAGAT CCGAAGTCTT CCTGCAGCCA T 471

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 180 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

ATGGCTGCAG GAAGACTTCG GATCTTGTTT CTGCTGTCC TGTCCTTGCA CCTGGGCCTT 60
 GGCTGGGTCC TTGATCTTCA AGAGGCTCCT GCGGCAGATG AGCTCTCATC TGGGAAAATG 120
 GCAGAGACTG GAAGGACCTG GAAGCCCAT CAGGGTAAOA ACAATGTCCG CCTTCCAAGA 180

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 180 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

TCTTGGAAGG CGGACATTGT TGTTACCCTG ATGGGGCTTC CAGGTCCTTC CAGTCTCTGC	60
CATTTTCCCA GATGAGAGCT CATCTGCCGC AGGAGCCTCT TGAAGATCAA GGACCCAGCC	120
AAGGCCCAGG TGCAAGGACA GGAGCAGCAG AAACAAGATC CGAAGTCTTC CTGCAGCCAT	180

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 291 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GCCTTACCTG GTTTGTGCCG GCTGTGGAGC CTGACCCTAC CAGTGGCTGA GCTTGGCCTG	60
GGCTATGCCT CAGAGGAGAA GATTATCTTC CGATACTGTG CTGGCAGCTG TCCCCAAGAG	120
GTCCGTACCC AGCACAGTCT GGTGCTGGCC CTTCTTCGAG GGCAGGGTCG AGCTCATGGC	180
AGACCTTGCT GCCAGCCCAC CAGCTATCCT GATGTGACCT TCCTTGATGA CCACCACCAT	240
TGGCAGCAGC TGCCTCAGCT CTCAGCCGCA GCTTGTGGCT GTGGTGGCTG A	291

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 291 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

TCAGCCACCA CAGCCACAAG CTGCGGCTGA GAGCTGAGGC AGCTGCTGCC AATGGTGGTG	60
GTCATCAAGG AAGGTCACAT CAGCATAGCT GGTGGGCTGG CAGCAAGGTC TGCCATGAGC	120
TCGACCCTGC CCTCGAAGAC GGGCCAGCAC CAGACTGTGC TGGGTACGGA CCTCTTGGGG	180
ACAGCTGCCA GCACAGTATC GGAAGATAAT CTTCTCCTCT GAGGCATAGC CCAGGCCAAG	240
CTCAGCCACT GGTAGGGTCA GGCTCCACAG CCGGCACAAA CCAGGTAAGG C	291

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Met Ala Ala Gly Arg Leu Arg Ile Leu Phe Leu Leu Leu Leu Ser Leu
 1 5 10 15

His Leu Gly Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Pro Ala Ala
 20 25 30

Asp Glu Leu Ser Ser Gly Lys Met Ala Glu Thr Gly Arg Thr Trp Lys
 35 40 45

Pro His Gln Gly Asn Asn Asn Val Arg Leu Pro Arg Ala Leu Pro Gly
 50 55 60

Leu Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu
 65 70 75 80

Gly Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser
 85 90 95

Cys Pro Gln Glu Val Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu
 100 105 110

Arg Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser
 115 120 125

Tyr Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu
 130 135 140

Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 145 150 155

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Met Ala Ala Gly Arg Leu Arg Ile Leu Phe Leu Leu Leu Leu Ser Leu
 1 5 10 15

His Leu Gly Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Pro Ala Ala
 20 25 30

Asp Glu Leu Ser Ser Gly Lys Met Ala Glu Thr Gly Arg Thr Trp Lys
 35 40 45

Pro His Gln Gly Asn Asn Asn Val Arg Leu Pro Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Ala Leu Pro Gly Leu Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala
 1 5 10 15
 Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr
 20 25 30
 Cys Ala Gly Ser Cys Pro Gln Glu Val Arg Thr Gln His Ser Leu Val
 35 40 45
 Leu Ala Arg Leu Arg Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys
 50 55 60
 Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp His His His
 65 70 75 80
 Trp Gln Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 85 90 95

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GCCCTGTCTG GTCCATGCCA GCTGTGGAGC CTGACCTGT CCGTGGCAGA GCTAGGCCTG 60
 GGCTACGCCT CAGAGGAGAA GGTCATCTTC CGCTACTGCG CCGGCAGCTG CCCCCGTGGT 120
 GCCCGCACCC AGCATGGCCT GGCCTGGCC CGGCTGCAGG GCCAGGGCCG AGCCACGGT 180
 GGGCCCTGCT GCCGGCCAC TCGCTACACC GACGTGGCCT TCCTCGATGA CCGCCACCGC 240
 TGGCAGCGGC TGCCCCAGCT CTCGGCGGCT GCCTGCGGCT GTGGTGGCTG A 291

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

```
TCAGCCACCA CAGCCGCAGG CAGCCGCCGA GAGCTGGGGC AGCCGCTGCC AGCGGTGGCG      60
GTCATCGAGG AAGGCCACGT CGGTGTAGCG AGTGGGCCCG CAGCAGGGCC CACCGTGGGC      120
TCGGCCCTGG CCCTGCAGCC GGGCCAGCGC CAGGCCATGC TGGGTGCGGG CACCACGGGG      180
GCAGCTGCCG GCGCAGTAGC GGAAGATGAC CTTCTCCTCT GAGGCGTAGC CCAGGCCTAG      240
CTCTGCCACG GACAGGGTCA GGCTCCACAG CTGGCATGGA CCAGACAGGG C          291
```

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

```
GCCCTGTCTG GTCCATGCCA GCTGTGGAGC CTGACCCTGT CCGTGGCAGA GCTAGGCCTG      60
GGCTACGCCT CAGAGGAGAA GGTCATCTTC CCTACTGCG CCGGCAGCTG CCCCCGTGGT      120
GCCCCACCCC AGCATGGCCT GGCGCTGGCC CGCTGCAGG GCCAGGGCCG AGCCCACGGC      180
GGGCCCTGCT GCCGGCCAC TCGCTACACC GACGTGGCCT TCCTCGATGA CCGCCACCGC      240
TGGCAGCGGC TGCCCCAGCT CTCGGCGGCT GCCTGCGGCT GTGGTGGCTG A          291
```

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

```
TCAGCCACCA CAGCCGCAGG CAGCCGCCGA GAGCTGGGGC AGCCGCTGCC AGCGGTGGCG      60
```

GTCATCGAGG AAGGCCACGT CGGTGTAGCG AGTGGGCCGG CAGCAGGGCC CGCCGTGGGC 120
 TCGGCCCTGG CCCTGCAGCC GGGCCAGCGC CAGGCCATGC TGGGTGCGGG CACCACGGGG 180
 GCAGCTGCCG GCGCAGTAGC GGAAGATGAC CTTCTCCTCT GAGGCGTAGC CCAGGCCTAG 240
 CTCTGCCACG GACAGGGTCA GGCTCCACAG CTGGCATGGA CCAGACAGGG C 291

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 471 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

ATGGCCGTAG GGAAGTTCCT GCTGGGCTCT CTGCTGCTCC TGTCCTGCA GCTGGGACAG 60
 GGCTGGGGCC CCGATGCCCG TGGGGTTCCC GTGGCCGATG GAGAGTTCTC GTCTGAACAG 120
 GTGGCAAAGG CTGGAGGGAC CTGGCTGGGC ACCCACCGCC CCCTTGCCCG CCTGCGCCGA 180
 GCCCTGTCTG GTCCATGCCA GCTGTGGAGC CTGACCCTGT CCGTGGCAGA GCTAGGCCTG 240
 GGCTACGCCT CAGAGGAGAA GGTCATCTTC CGCTACTGCG CCGGCAGCTG CCCCCGTGGT 300
 GCGCGACCC AGCATGGCCT GGCGCTGGCC CGGCTGCAGG GCCAGGGCCG AGCCACGGT 360
 GGGCCCTGCT GCCGGCCAC TCGCTACACC GACGTGGCCT TCCTCGATGA CCGCCACCGC 420
 TGCGAGCGGC TGCCCCAGCT CTCGGGCTCT GCCTGCGGCT GTGGTGGCTG A 471

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 471 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TCAGCCACCA CAGCCGAGG CAGCCGCCGA GAGCTGGGGC AGCCGCTGCC AGCGGTGGCG 60
 GTCATCGAGG AAGGCCACGT CGGTGTAGCG AGTGGGCCGG CAGCAGGGCC CACCGTGGGC 120
 TCGGCCCTGG CCCTGCAGCC GGGCCAGCGC CAGGCCATGC TGGGTGCGGG CACCACGGGG 180
 GCAGCTGCCG GCGCAGTAGC GGAAGATGAC CTTCTCCTCT GAGGCGTAGC CCAGGCCTAG 240
 CTCTGCCACG GACAGGGTCA GGCTCCACAG CTGGCATGGA CCAGACAGGG CTCGGCGCAG 300
 GCGGGCAAGG GGGCGGTGGG TGCCAGCCA GGTCCCTCCA GCCTTTGCCA CCTGTTGAGA 360

CGAGAACTCT CCATCGGCCA CGGGAACCCC ACGGGCATCG GGGCCCCAGC CCTGTCCCAG 420
 CTGCAGGGAC AGGAGCAGCA GAGAGCCCAG CAGGAACTTC CCTACGGCCA T 471

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 471 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

ATGGCCGTAG GGAAGTTCCT GCTGGGCTCC CTGCTGCTCC TGTCCCTGCA GCTGGGACAG 60
 GGCTGGGGCC CCGATGCCCG TGGGGTTCCC GTGGCCGATG GAGAGTTCTC GTCTGAACAG 120
 GTGGCAAAGG CTGGAGGGAC CTGGCTGGGC ACCACCGCC CCCTTGCCCG CCTGCGCCGA 180
 GCCCTGTCTG GTCCATGCCA GCTGTGGAGC CTGACCCTGT CCGTGGCAGA GCTAGGCCTG 240
 GGCTACGCCT CAGAGGAGAA GGTCATCTTC CGTACTGCG CCGGCAGCTG CCCCCGTGGT 300
 GCGCGACCC AGCATGGCCT GCGCTGGCC CGGTGCAGG GCCAGGGCCG AGCCCACGGC 360
 GGGCCCTGCT GCCGGCCAC TCGTACACC GACGTGGCCT TCCTCGATGA CCGCCACCGC 420
 TGGCAGCGGC TGCCCCAGCT CTCGGCGGCT GCCTGGCGCT GTGGTGGCTG A 471

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 471 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TCAGCCACCA CAGCCGCAGG CAGCCGCCGA GAGCTGGGGC AGCCGCTGCC AGCGGTGGCG 60
 GTCATCGAGG AAGGCCACGT CGGTGTAGCG AGTGGGCGG CAGCAGGGCC CGCCGTGGGC 120
 TCGGCCCTGG CCCTGCAGCC GGGCCAGCGC CAGGCCATGC TGGGTGCGGG CACCACGGGG 180
 GCAGCTGCCG GCGCAGTAGC GGAAGATGAC CTTCTCCTCT GAGGCGTAGC CCAGGCCTAG 240
 CTCTGCCACG GACAGGGTCA GGCTCCACAG CTGGCATGGA CCAGACAGGG CTCGGCGCAG 300
 GCGGGCAAGG GGGCGGTGGG TGCCAGCCA GGTCCCTCCA GCCTTTGCCA CCTGTTTACA 360
 CGAGAACTCT CCATCGGCCA CGGGAACCCC ACGGGCATCG GGGCCCCAGC CCTGTCCCAG 420
 CTGCAGGGAC AGGAGCAGCA GGGAGCCCAG CAGGAACTTC CCTACGGCCA T 471

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

ATGGCCGTAG GGAAGTTCCT GCTGGGCTCT CTGCTGCTCC TGTCCCTGCA GCTGGGACAG 60
GGCTGGGGC 69

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

GCCCCAGCCC TGTCCAGCT GCAGGGACAG GAGCAGCAGA GAGCCCAGCA GGAAGTTCCTCC 60
TACGGCCAT 69

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

ATGGCCGTAG GGAAGTTCCT GCTGGGCTCC CTGCTGCTCC TGTCCCTGCA GCTGGGACAG 60
GGCTGGGGC 69

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GCCCCAGCCC TGTCOCAGCT GCAGGGACAG GAGCAGCAGG GAGCCCAGCA GGAACCTCCC 60
TACGGCCAT 69

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

CCCGATGCCC GTGGGGTTCC CGTGGCCGAT GGAGAGTTCT CGTCTGAACA GGTGGCAAAG 60
GCTGGAGGGA CCTGGCTGGG CACCCACCGC CCCCTTGCCC GCCTGCGCCG A 111

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

TCGGCGCAGG CGGGCAAGGG GGCGGTGGGT GCCCAGCCAG GTCCCTCCAG CCTTTGCCAC 60
CTGTTTCAGAC GAGAACTCTC CATCGGCCAC GGAACCCCA CGGGCATCGG G 111

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ATGGCCGTAG GGAAGTTCTT GCTGGGCTCT CTGCTGCTCC TGTCCCTGCA GCTGGGACAG 60
GGCTGGGGCC CCGATGCCCG TGGGGTCCCC GTGGCCGATG GAGAGTTCTC GTCTGAACAG 120

GTGGCAAAGG CTGGAGGGAC CTGGCTGGGC ACCCACC GCC CCCTTGCCCG CCTGCGCCGA 180

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

TCGGCGCAGG CGGGCAAGGG GCGGTGGGT GCCAGCCAG GTCCCTCCAG CCTTTGCCAC 60
 CTGTTTCAGAC GAGAACTCTC CATCGGCCAC GGAACCCCA CGGCATCGG GGCCCCAGCC 120
 CTGTCCCAGC TGCAGGGACA GGAGCAGCAG AGAGCCCAGC AGGAACTTCC CTACGGCCAT 180

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

ATGGCCGTAG GGAAGTTCCT GCTGGGCTCC CTGCTGCTCC TGTCCTGCA GCTGGGACAG 60
 GGCTGGGGCC CCGATGCCCG TGGGGTTCCG GTGGCCGATG GAGAGTTCTC GTCTGAACAG 120
 GTGGCAAAGG CTGGAGGGAC CTGGCTGGGC ACCCACC GCC CCCTTGCCCG CCTGCGCCGA 180

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

TCGGCGCAGG CGGGCAAGGG GCGGTGGGT GCCAGCCAG GTCCCTCCAG CCTTTGCCAC 60
 CTGTTTCAGAC GAGAACTCTC CATCGGCCAC GGAACCCCA CGGCATCGG GGCCCCAGCC 120
 CTGTCCCAGC TGCAGGGACA GGAGCAGCAG GGAGCCCAGC AGGAACTTCC CTACGGCCAT 180

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

```

Met Ala Val Gly Lys Phe Leu Leu Gly Ser Leu Leu Leu Leu Ser Leu
 1           5           10           15
Gln Leu Gly Gln Gly Trp Gly Pro Asp Ala Arg Gly Val Pro Val Ala
 20           25           30
Asp Gly Glu Phe Ser Ser Glu Gln Val Ala Lys Ala Gly Gly Thr Trp
 35           40           45
Leu Gly Thr His Arg Pro Leu Ala Arg Leu Arg Arg Ala Leu Ser Gly
 50           55           60
Pro Cys Gln Leu Trp Ser Leu Thr Leu Ser Val Ala Glu Leu Gly Leu
 65           70           75           80
Gly Tyr Ala Ser Glu Gln Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser
 85           90           95
Cys Pro Arg Gly Ala Arg Thr Gln His Gly Leu Ala Leu Ala Arg Leu
100           105           110
Gln Gly Gln Gly Arg Ala His Gly Gly Pro Cys Cys Arg Pro Thr Arg
115           120           125
Tyr Thr Asp Val Ala Phe Leu Asp Asp Arg His Arg Trp Gln Arg Leu
130           135           140
Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
145           150           155

```

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

```

Met Ala Val Gly Lys Phe Leu Leu Gly Ser Leu Leu Leu Leu Ser Leu
 1           5           10           15
Gln Leu Gly Gln Gly Trp Gly Pro Asp Ala Arg Gly Val Pro Val Ala
 20           25           30

```

Asp Gly Glu Phe Ser Ser Glu Gln Val Ala Lys Ala Gly Gly Thr Trp
 35 40 45

Leu Gly Thr His Arg Pro Leu Ala Arg Leu Arg Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Met Ala Val Gly Lys Phe Leu Leu Gly Ser Leu Leu Leu Leu Ser Leu
 1 5 10 15

Gln Leu Gly Gln Gly Trp Gly
 20

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Pro Asp Ala Arg Gly Val Pro Val Ala Asp Gly Glu Phe Ser Ser Glu
 1 5 10 15

Gln Val Ala Lys Ala Gly Gly Thr Trp Leu Gly Thr His Arg Pro Leu
 20 25 30

Ala Arg Leu Arg Arg
 35

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Ala Leu Ser Gly Pro Cys Gln Leu Trp Ser Leu Thr Leu Ser Val Ala
 1 5 10 15
 Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr
 20 25 30
 Cys Ala Gly Ser Cys Pro Arg Gly Ala Arg Thr Gln His Gly Leu Ala
 35 40 45
 Leu Ala Arg Leu Gln Gly Gln Gly Arg Ala His Gly Gly Pro Cys Cys
 50 55 60
 Arg Pro Thr Arg Tyr Thr Asp Val Ala Phe Leu Asp Asp Arg His Arg
 65 70 75 80
 Trp Gln Arg Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 85 90 95

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

TGCCAGCTGT GGAGCCTGAC CCTGTCCGTG GCAGAGCTAG GCCTGGGCTA CGCCTCAGAG 60
 GAGAAGGTCA TCTTCCGCTA CTGCGCCGGC AGTGCCCCC GTGGTGCCCG CACCCAGCAT 120
 GGCCTGGCGC TGGCCCGGCT GCAGGGCCAG GCGCGAGCCC ACGGTGGGCC CTGCTGCCGG 180
 CCCACTCGCT ACACCGACGT GGCCTTCCTC GATGACCGCC ACCGCTGGCA GCGGCTGCCC 240
 CAGCTCTCGG CGGCTGCCTG CGGCTGT 267

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Cys Gln Leu Trp Ser Leu Thr Leu Ser Val Ala Glu Leu Gly Leu Gly
 1 5 10 15
 Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser Cys
 20 25 30
 Pro Arg Gly Ala Arg Thr Gln His Gly Leu Ala Leu Ala Arg Leu Gln
 35 40 45

Gly Gln Gly Arg Ala His Gly Gly Pro Cys Cys Arg Pro Thr Arg Tyr
 50 55 60
 Thr Asp Val Ala Phe Leu Asp Asp Arg His Arg Trp Gln Arg Leu Pro
 65 70 75 80
 Gln Leu Ser Ala Ala Ala Cys Gly Cys
 85

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Ala Leu Ser Gly Pro
 1 5

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GTSASYGASY TGGGYCTGGG CTAY

24

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

TTYMGSTACT GCRSMGGCKC YTGC

24

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

RWAGGCSRTS GKGCKGCARC AKGS

24

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

MKCRTCYARR AASGACASST C

21

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 168 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

CGGCTTGTGA CCGAGCTGGG CCTGGGCTAC GCCTCAGAGG AGAAGGTCAT CTTCCGCTAC

60

TGCGCCGGCA GCTGCCCCCG TGGTGCCCCG ACCCAGCATG GCCTGGCGCT GGCCCGGCTG

120

CAGGGCCAGG GCCGAGCCCA CGGCGGGCCC TGCTGCCGCC CCATGGCC

168

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GAGGAGAAGG TCATCTTCCG

20

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

GCCGTGGGCT CGGCCCTGGC

20

(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

AGAGGAGAAG GTCATCTTCC GCTA

24

(2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

CTCGGCCCTG GCCCTGCAGC

20

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

TGCAGCCGGG CCAGCGCCAG

20

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

CGCGGATCCA TGCCTGGATT CGAGGGTGCA G

31

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

CGCGGATCCA TGGCCGTAGG GAAGTTCCTG C

31

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

CTCCCAAGCT TTTACTTGTC ATCGTCGTCC TTGTAGTCGC CACCACAGCC GCAGGCAGCC

60

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

CTCCCAAGCT TTTACTTGTC ATCGTCGTCC TTGTAGTCTC GAGGAAGGCC ACGTCGGTG

59

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

TCAGCCACCA CAGCCGCAGG CAGCC

25